

## SEQUENCE LISTING

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WATAHIKI, Masanori

<120> RNA Polymerase

<130> 024705-077

<140> US 09/254,344

<141> 1999-09-03

<150> PCT/JP98/03037

<151> 1998-07-06

<150> JP 9/180883

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Glu Glu Gln Leu Asn Lys Arg Val Gly His Val Tyr Lys Lys Ala Phe  
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Lys Phe Ile Glu Glu Asn His Glu Asn Ile Met Ala Cys Ala Lys Ser  
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Cys Phe Glu Tyr Ala Gly Val Gln His His Gly Leu Ser Tyr Asn Cys  
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 Ser Thr Asn Met Thr Thr Ile Gln Ala Ala Ala Gly Met Leu Gly Lys  
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 Lys His Phe Lys Lys His Val Glu Glu Gln Leu Asn Lys Arg His Gly  
 165 170 175  
 Gln Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Ile  
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Asp His Glu Ala Leu Gln Leu Ala Gln Glu Tyr Val Asp Val Leu Ala  
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Arg His Arg Cys Ala Val His Trp Thr Thr Pro Asp Gly Phe Pro Val  
                     725                    730                    735

Trp Gln Glu Tyr Arg Lys Pro Leu Gln Lys Arg Leu Asp Met Ile Phe  
                     740                    745                    750

Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr Leu Lys Asp Ser  
                     755                    760                    765

Gly Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val  
                     770                    775                    780

His Ser Gln Asp Gly Ser His Leu Arg Met Thr Val Val Tyr Ala His  
                     785                    790                    795                    800

Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe Gly  
                     805                    810                    815

Thr Ile Pro Ala Asp Ala Gly Lys Leu Phe Lys Ala Val Arg Glu Thr  
                     820                    825                    830

Met Val Ile Thr Tyr Glu Asn Asn Asp Val Leu Ala Asp Phe Tyr Ser  
                     835                    840                    845

Gln Phe Ala Asp Gln Leu His Glu Thr Gln Leu Asp Lys Met Pro Pro  
                     850                    855                    860

Leu Pro Lys Lys Gly Asn Leu Asn Leu Gln Asp Ile Leu Lys Ser Asp  
                     865                    870                    875                    880

Phe Ala Phe Ala

<210> 5

<211> 906

<212> PRT

<213> Bacteriophage K11

<220>

<221> VARIANT

<222> 77, 78, 79, 157, 158, 159, 236, 237, 238, 456, 457, 458,  
 533, 534, 535, 608, 609, 610, 687, 688, 689, 762, 763, 764,  
 842, 843, 844

<223> Xaa = Any Amino Acid

<400> 5

Met Asn Ala Leu Asn Ile Gly Arg Asn Asp Phe Ser Glu Ile Glu Leu



1	5	10	15
Ala Ala Ile Pro Tyr Asn Ile Leu Ser Glu His Tyr Gly Asp Gln Ala	20	25	30
Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ala Tyr Glu Leu Gly Arg	35	40	45
Gln Arg Phe Leu Lys Met Leu Glu Arg Gln Val Lys Ala Gly Glu Phe	50	55	60
Ala Asp Asn Ala Ala Ala Lys Pro Leu Val Leu Thr Xaa Xaa Xaa Gln	65	70	75
Leu Thr Lys Arg Ile Asp Asp Trp Lys Glu Glu Gln Ala Asn Ala Arg	85	90	95
Gly Lys Lys Pro Arg Ala Tyr Tyr Pro Ile Lys His Gly Val Ala Ser	100	105	110
Glu Leu Ala Val Ser Met Gly Ala Glu Val Leu Lys Glu Lys Arg Gly	115	120	125
Val Ser Ser Glu Ala Ile Ala Leu Leu Thr Ile Lys Val Val Leu Gly	130	135	140
Asn Ala His Arg Pro Leu Lys Gly His Asn Pro Ala Xaa Xaa Xaa Gln	145	150	155
Leu Gly Lys Ala Leu Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Glu	165	170	175
Gln Glu Ala Ala Tyr Phe Lys Lys Asn Val Ala Asp Gln Leu Asp Lys	180	185	190
Arg Val Gly His Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala	195	200	205
Asp Met Ile Ser Lys Gly Met Leu Gly Gly Asp Asn Trp Ala Ser Trp	210	215	220
Lys Thr Asp Glu Gln Met His Val Gly Thr Lys Xaa Xaa Xaa Leu Leu	225	230	235
Ile Glu Gly Thr Gly Leu Val Glu Met Thr Lys Asn Lys Met Ala Asp	245	250	255

Gly Ser Asp Asp Val Thr Ser Met Gln Met Val Gln Leu Ala Pro Ala  
 260 265 270

Phe Val Glu Leu Leu Ser Lys Arg Ala Gly Ala Leu Ala Gly Ile Ser  
 275 280 285

Pro Met His Gln Pro Cys Val Val Pro Pro Lys Pro Trp Val Glu Thr  
 290 295 300

Val Gly Gly Gly Tyr Trp Ser Val Gly Arg Arg Pro Leu Ala Leu Val  
 305 310 315 320

Arg Thr His Ser Lys Lys Ala Leu Arg Arg Tyr Ala Asp Val His Met  
 325 330 335

Pro Glu Val Tyr Lys Ala Val Asn Leu Ala Gln Asn Thr Pro Trp Lys  
 340 345 350

Val Asn Lys Lys Val Leu Ala Val Val Asn Glu Ile Val Asn Trp Lys  
 355 360 365

His Cys Pro Val Gly Asp Val Pro Ala Ile Glu Arg Glu Glu Leu Pro  
 370 375 380

Pro Arg Pro Asp Asp Ile Asp Thr Asn Glu Val Ala Arg Lys Ala Trp  
 385 390 395 400

Arg Lys Glu Ala Ala Ala Val Tyr Arg Lys Asp Lys Ala Arg Gln Ser  
 405 410 415

Arg Arg Cys Arg Cys Glu Phe Met Val Ala Gln Ala Asn Lys Phe Ala  
 420 425 430

Asn His Lys Ala Ile Trp Phe Pro Tyr Asn Met Asp Trp Arg Gly Arg  
 435 440 445

Val Tyr Ala Val Ser Met Phe Xaa Xaa Xaa Gly Asn Asp Met Thr Lys  
 450 455 460

Gly Ser Leu Thr Leu Ala Lys Gly Lys Pro Ile Gly Leu Asp Gly Phe  
 465 470 475 480

Tyr Trp Leu Lys Ile His Gly Ala Asn Cys Ala Gly Val Asp Lys Val  
 485 490 495

Pro Phe Pro Glu Arg Ile Lys Phe Ile Glu Glu Asn Glu Gly Asn Ile  
 500 505 510

Leu Ala Ser Ala Ala Asp Pro Leu Asn Asn Thr Trp Trp Thr Gln Gln  
 515 520 525

Asp Ser Pro Phe Xaa Xaa Xaa Ala Phe Cys Phe Glu Tyr Ala Gly Val  
 530 535 540

Lys His His Gly Leu Asn Tyr Asn Cys Ser Leu Pro Leu Ala Phe Asp  
 545 550 555 560

Gly Ser Cys Ser Gly Ile Gln His Phe Ser Ala Met Leu Arg Asp Ser  
 565 570 575

Ile Gly Gly Arg Ala Val Asn Leu Leu Pro Ser Asp Thr Val Gln Asp  
 580 585 590

Ile Tyr Lys Ile Val Ala Asp Lys Val Asn Glu Val Leu His Gln Xaa  
 595 600 605

Xaa Xaa Asn Gly Ser Gln Thr Val Val Glu Gln Ile Ala Asp Lys Glu  
 610 615 620

Thr Gly Glu Phe His Glu Lys Val Thr Leu Gly Glu Ser Val Leu Ala  
 625 630 635 640

Ala Gln Trp Leu Gln Tyr Gly Val Thr Arg Lys Val Thr Lys Arg Ser  
 645 650 655

Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Ser Leu Val Arg Gln Gln  
 660 665 670

Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Asn Gly Glu Xaa Xaa  
 675 680 685

Xaa Phe Thr His Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile  
 690 695 700

Trp Asp Ala Val Thr Val Thr Val Val Ala Ala Val Glu Ala Met Asn  
 705 710 715 720

Trp Leu Lys Ser Ala Ala Lys Leu Leu Ala Ala Glu Val Lys Asp Lys  
 725 730 735

Lys Thr Lys Glu Val Leu Arg Lys Arg Cys Ala Ile His Trp Val Thr  
                   740                  745                  750

Pro Asp Gly Phe Pro Val Trp Gln Glu Xaa Xaa Xaa Gln Asn Gln Ala  
                   755                  760                  765

Arg Leu Lys Leu Val Phe Leu Gly Gln Ala Asn Val Lys Met Thr Tyr  
                   770                  775                  780

Asn Thr Gly Lys Asp Ser Glu Ile Asp Ala His Lys Gln Glu Ser Gly  
                   785                  790                  795                  800

Ile Ala Pro Asn Phe Val His Ser Gln Asp Gly Ser His Leu Arg Met  
                   805                  810                  815

Thr Val Val His Ala Asn Glu Val Tyr Gly Ile Asp Ser Phe Ala Leu  
                   820                  825                  830

Ile His Asp Ser Ser Gly Thr Ile Pro Xaa Xaa Xaa Gly Asn Leu Phe  
                   835                  840                  845

Lys Ala Val Arg Glu Thr Met Val Lys Thr Tyr Glu Asp Asn Asp Val  
                   850                  855                  860

Ile Ala Asp Phe Tyr Asp Gln Phe Ala Asp Gln Leu His Glu Ser Gln  
                   865                  870                  875                  880

Leu Asp Lys Met Pro Ala Val Pro Ala Lys Gly Asp Leu Asn Leu Arg  
                   885                  890                  895

Asp Ile Leu Glu Ser Asp Phe Ala Phe Ala  
                   900                  905

<210> 6

<211> 874

<212> PRT

<213> Bacteriophage SP6

<220>

<221> VARIANT

<222> 49, 50, 51, 107, 108, 109, 186, 187, 188, 265, 266, 267,  
 344, 345, 346, 424, 425, 426, 504, 505, 506, 579, 580, 657,  
 658, 659, 737, 738, 739, 813, 814, 815

<223> Xaa = Any Amino Acid

<400> 6

Met Gln Asp Leu His Ala Ile Gln Leu Gln Leu Glu Glu Glu Met Phe

1	5	10	15
Asn Gly Gly Ile Arg Arg Phe Glu Ala Asp Gln Gln Arg Gln Ile Ala	20	25	30
Ala Gly Ser Glu Ser Asp Thr Ala Trp Asn Arg Arg Leu Leu Ser Glu	35	40	45
Xaa Xaa Xaa Pro Met Ala Glu Gly Ile Gln Ala Tyr Lys Glu Glu Tyr	50	55	60
Glu Gly Lys Lys Gly Arg Ala Pro Arg Ala Leu Ala Phe Leu Gln Cys	65	70	75
Val Glu Asn Glu Val Ala Ala Tyr Ile Thr Met Lys Val Val Met Asp	85	90	95
Met Leu Asn Thr Asp Ala Thr Leu Gln Ala Xaa Xaa Xaa Ser Val Ala	100	105	110
Glu Arg Ile Glu Asp Gln Val Arg Phe Ser Lys Leu Glu Gly His Ala	115	120	125
Ala Lys Tyr Phe Glu Lys Val Lys Lys Ser Leu Lys Ala Ser Arg Thr	130	135	140
Lys Ser Tyr Arg His Ala His Asn Val Ala Val Val Ala Glu Lys Ser	145	150	155
Val Ala Glu Lys Asp Ala Asp Phe Asp Arg Trp Glu Ala Trp Pro Lys	165	170	175
Glu Thr Gln Leu Gln Ile Gly Thr Thr Xaa Xaa Xaa Ile Leu Glu Gly	180	185	190
Ser Val Phe Tyr Asn Gly Glu Pro Val Phe Met Arg Ala Met Arg Thr	195	200	205
Tyr Gly Gly Lys Thr Ile Tyr Tyr Leu Gln Thr Ser Glu Ser Val Gly	210	215	220
Gln Trp Ile Ser Ala Phe Lys Glu His Val Ala Gln Leu Ser Pro Ala	225	230	235
			240

Tyr Ala Pro Cys Val Ile Pro Pro Arg Pro Trp Arg Thr Pro Phe Asn  
 245 250 255  
 Gly Gly Phe His Thr Glu Lys Val Xaa Xaa Xaa Ile Arg Leu Val Lys  
 260 265 270  
 Gly Asn Arg Glu His Val Arg Lys Leu Thr Gln Lys Gln Met Pro Lys  
 275 280 285  
 Val Tyr Lys Ala Ile Asn Ala Leu Gln Asn Thr Gln Trp Gln Ile Asn  
 290 295 300  
 Lys Asp Val Leu Ala Val Ile Glu Glu Val Ile Arg Leu Asp Leu Gly  
 305 310 315 320  
 Tyr Gly Val Pro Ser Phe Lys Pro Leu Ile Asp Lys Glu Asn Lys Pro  
 325 330 335  
 Ala Asn Pro Val Pro Val Glu Xaa Xaa Xaa Leu Arg Gly Arg Glu Leu  
 340 345 350  
 Lys Glu Met Leu Ser Pro Glu Gln Trp Gln Gln Phe Ile Asn Trp Lys  
 355 360 365  
 Gly Glu Cys Ala Arg Leu Tyr Thr Ala Glu Thr Lys Arg Gly Ser Lys  
 370 375 380  
 Ser Ala Ala Val Val Arg Met Val Gly Gln Ala Arg Lys Tyr Ser Ala  
 385 390 395 400  
 Phe Glu Ser Ile Tyr Phe Val Tyr Ala Met Asp Ser Arg Ser Arg Val  
 405 410 415  
 Tyr Val Gln Ser Ser Thr Leu Xaa Xaa Xaa Ser Asn Asp Leu Gly Lys  
 420 425 430  
 Ala Leu Leu Arg Phe Thr Glu Gly Arg Pro Val Asn Gly Val Glu Ala  
 435 440 445  
 Leu Lys Trp Phe Cys Ile Asn Gly Ala Asn Leu Trp Gly Trp Asp Lys  
 450 455 460  
 Lys Thr Phe Asp Val Arg Val Ser Asn Val Leu Asp Glu Glu Phe Gln  
 465 470 475 480

Asp Met Cys Arg Asp Ile Ala Ala Asp Pro Leu Thr Phe Thr Gln Trp  
 485 490 495

Ala Lys Ala Asp Ala Pro Tyr Xaa Xaa Xaa Ala Trp Cys Phe Glu Tyr  
 500 505 510

Ala Gln Tyr Leu Asp Leu Val Asp Glu Gly Arg Ala Asp Glu Phe Arg  
 515 520 525

Thr His Leu Pro Val His Gln Asp Gly Ser Cys Ser Gly Ile Gln His  
 530 535 540

Tyr Ser Ala Met Leu Arg Asp Glu Val Gly Ala Lys Ala Val Asn Leu  
 545 550 555 560

Lys Pro Ser Asp Ala Pro Gln Asp Ile Tyr Gly Ala Val Ala Gln Val  
 565 570 575

Val Ile Xaa Xaa Asn Ala Leu Tyr Met Asp Ala Asp Asp Ala Thr Thr  
 580 585 590

Phe Thr Ser Gly Ser Val Thr Leu Ser Gly Thr Glu Leu Arg Ala Met  
 595 600 605

Ala Ser Ala Trp Asp Ser Ile Gly Ile Thr Arg Ser Leu Thr Lys Lys  
 610 615 620

Pro Val Met Thr Leu Pro Tyr Gly Ser Thr Arg Leu Thr Cys Arg Glu  
 625 630 635 640

Ser Val Ile Asp Tyr Ile Val Asp Leu Glu Glu Lys Glu Ala Gln Lys  
 645 650 655

Xaa Xaa Xaa Glu Gly Arg Thr Ala Asn Lys Val His Pro Phe Glu Asp  
 660 665 670

Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala Tyr Asn Tyr Met Thr  
 675 680 685

Ala Leu Ile Trp Pro Ser Ile Ser Glu Val Val Lys Ala Pro Ile Val  
 690 695 700

Ala Met Lys Met Ile Arg Gln Leu Ala Arg Phe Ala Ala Lys Arg Asn  
 705 710 715 720

Glu Gly Leu Met Tyr Thr Leu Pro Thr Gly Phe Ile Leu Glu Gln Lys  
                             725                            730                            735

Xaa Xaa Xaa Thr Glu Met Leu Arg Val Arg Thr Cys Leu Met Gly Asp  
                             740                            745                            750

Ile Lys Met Ser Leu Gln Val Glu Thr Asp Ile Val Asp Glu Ala Ala  
                             755                            760                            765

Met Met Gly Ala Ala Ala Pro Asn Phe Val His Gly His Asp Ala Ser  
                             770                            775                            780

His Leu Ile Leu Thr Val Cys Glu Leu Val Asp Lys Gly Val Thr Ser  
                             785                            790                            795                            800

Ile Ala Val Ile His Asp Ser Phe Gly Thr His Ala Xaa Xaa Xaa Leu  
                             805                            810                            815

Thr Leu Arg Val Ala Leu Lys Gly Gln Met Val Ala Met Tyr Ile Asp  
                             820                            825                            830

Gly Asn Ala Leu Gln Lys Leu Leu Glu Glu His Glu Val Arg Trp Met  
                             835                            840                            845

Val Asp Thr Gly Ile Glu Val Pro Glu Gln Gly Glu Phe Asp Leu Asn  
                             850                            855                            860

Glu Ile Met Asp Ser Glu Tyr Val Phe Ala  
                             865                            870

<210> 7  
 <211> 78  
 <212> PRT  
 <213> Bacteriophage T7

<400> 7  
 Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala  
 1                            5                            10                            15

Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr  
                             20                            25                            30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro  
                             35                            40                            45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser  
                             50                            55                            60



Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys  
 65 70 75

<210> 8  
 <211> 78  
 <212> PRT  
 <213> Bacteriophage T7

<220>  
 <221> PEPTIDE  
 <222> (1)..(78)  
 <223> Mutant T7 RNA polymerase F644Y.

<400> 8  
 Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala  
 1 5 10 15

Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln Gln Val Leu Glu Asp Thr  
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro  
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Thr Trp Glu Ser Val Ser  
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys  
 65 70 75

<210> 9  
 <211> 78  
 <212> PRT  
 <213> Bacteriophage T7

<220>  
 <221> PEPTIDE  
 <222> (1)..(78)  
 <223> Mutant T7 RNA polymerase F646Y.

<400> 9  
 Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala  
 1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Tyr Arg Gln Gln Val Leu Glu Asp Thr  
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro  
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser  
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys  
 65 70 75

<210> 10

<211> 78  
 <212> PRT  
 <213> Bacteriophage T7

<220>  
 <221> PEPTIDE  
 <222> (1)..(78)  
 <223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 10  
 Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala  
 1 5 10 15  
 Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr  
 20 25 30  
 Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Pro Met Tyr Thr Gln Pro  
 35 40 45  
 Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser  
 50 55 60  
 Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys  
 65 70 75

<210> 11  
 <211> 73  
 <212> PRT  
 <213> Bacteriophage T7

<400> 11  
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg  
 1 5 10 15  
 Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln  
 20 25 30  
 Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly  
 35 40 45  
 Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu  
 50 55 60  
 Ile Trp Glu Ser Val Ser Val Thr Val  
 65 70

<210> 12  
 <211> 73  
 <212> PRT  
 <213> Bacteriophage T7

<220>  
 <221> PEPTIDE  
 <222> (1)..(73)  
 <223> Mutant T7 RNA polymerase F644Y.

<400> 12

Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg  
 1 5 10 15  
 Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln  
 20 25 30  
 Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly  
 35 40 45  
 Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu  
 50 55 60  
 Ile Trp Glu Ser Val Ser Val Thr Val  
 65 70

<210> 13  
 <211> 73  
 <212> PRT  
 <213> Bacteriophage T7  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(73)  
 <223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 13  
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg  
 1 5 10 15  
 Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln  
 20 25 30  
 Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly  
 35 40 45  
 Pro Met Tyr Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu  
 50 55 60  
 Ile Trp Glu Ser Val Ser Val Thr Val  
 65 70

<210> 14  
 <211> 73  
 <212> PRT  
 <213> Bacteriophage T3

<400> 14  
 Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg  
 1 5 10 15  
 Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln  
 20 25 30  
 Gln Val Leu Asp Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly  
 35 40 45  
 Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu  
 50 55 60

Ile Trp Asp Ala Val Ser Val Thr Val  
65 70

<210> 15  
<211> 73  
<212> PRT  
<213> Bacteriophage K11

<400> 15  
Ala Ala Gln Trp Leu Gln Tyr Gly Val Thr Arg Lys Val Thr Lys Arg  
1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Ser Leu Val Arg Gln  
20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Asn Gly Glu Gly  
35 40 45

Leu Met Phe Thr His Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu  
50 55 60

Ile Trp Asp Ala Val Thr Val Thr Val  
65 70

<210> 16  
<211> 75  
<212> PRT <  
213> Bacteriophage SP6

<400> 16  
Ala Ser Ala Trp Asp Ser Ile Gly Ile Thr Arg Ser Leu Thr Lys Lys  
1 5 10 15

Pro Val Met Thr Leu Pro Tyr Gly Ser Thr Arg Leu Thr Cys Arg Glu  
20 25 30

Ser Val Ile Asp Tyr Ile Val Asp Leu Glu Glu Lys Glu Ala Gln Lys  
35 40 45

Ala Val Ala Glu Gly Arg Thr Ala Asn Lys Val His Pro Phe Glu Asp  
50 55 60

Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala  
65 70 75

<210> 17  
<211> 31  
<212> DNA  
<213> Bacteriophage T7

<220>  
<221> misc\_feature  
<222> (1)..(31)  
<223> Mutant T7 RNA polymerase wild type.

<220>

<221> misc\_feature  
 <222> (25)..(25)  
 <223> Nucleotide 25 is "n" wherein "n" = any nucleotide.

<400> 17  
 gggagggggg ggggggggcc cccnngggcg t 31

<210> 18  
 <211> 32  
 <212> DNA  
 <213> Bacteriophage T7

<220>  
 <221> misc\_feature  
 <222> (1)..(32)  
 <223> Mutant T7 RNA polymerase wild type.

<220>  
 <221> misc\_feature  
 <222> (1)..(32)  
 <223> Nucleotides 6-8, 18, 25-30 are "n" wherein "n" = any nucleotide.

<400> 18  
 gcgtcnnnaa aacgcacntt ttctntcgtn gg 32

<210> 19  
 <211> 19  
 <212> DNA  
 <213> Bacteriophage T7

<220>  
 <221> misc\_feature  
 <222> (1)..(19)  
 <223> Mutant T7 RNA polymerase F644Y.

<400> 19  
 cgaggggggg ccggtaccc 19

<210> 20  
 <211> 25  
 <212> DNA  
 <213> Bacteriophage T7

<220>  
 <221> misc\_feature  
 <222> (1)..(25)  
 <223> Mutant T7 RNA polymerase F644Y.

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> Nucleotide 6 is "n" wherein "n" = any nucleotide.

<400> 20  
 cccctntttg ttcctttagt gaggt 25

<210> 21  
 <211> 18  
 <212> DNA  
 <213> Bacteriophage T7

<220>  
 <221> misc\_feature  
 <222> (1)..(18)  
 <223> Mutant T7 RNA polymerase F667Y.

<400> 21  
 gagggggggcc ggtaacgc

18

<210> 22  
 <211> 22  
 <212> DNA  
 <213> Bacteriophage T7

<220>  
 <221> misc\_feature  
 <222> (1)..(22)  
 <223> Mutant T7 RNA polymerase F667Y.

<400> 22  
 acgccttttg ttcccttttag tg

22

<210> 23  
 <211> 569  
 <212> DNA  
 <213> Bacteriophage T7

<220>  
 <221> misc\_feature  
 <222> (1)..(569)  
 <223> Mutant T7 RNA polymerase F644Y/L665P/F667Y.

<220>  
 <221> misc\_feature  
 <222> (1)..(472)  
 <223> Nucleotides 1-14, 17-18, 21, 26, 29, 34, 38, 40, 50-51, 53, 58, 7  
 5-76, 85, 110, 117, 132, 142, 150, 157, 399, 440 and 472 are "n"  
 wherein "n" = any nucleotide

<400> 23  
 nnnnnnnnnn nnnnggnngt nggttncgna tccnaaangn aacaggggggn nantgtgnaa 60  
 acatgaatat ttttnntaag ctttnattcc agggcaagac attttaaccn aaattgncaa 120  
 attatatcac tnattagaca gnaaaatctn acccagntaa gacttctgga ggtttggtac 180  
 agtagtttgt cttggatgct tcatgtatgc agtcacttat agtcagtatt gcacttggca 240  
 cacttcagct taaaccaaca ggataggaaa aatagggagc aacatggagt ggcatcctgg 300  
 tattttctaca gtcctgtaga tgaagtctct atatgtgcaa catcctggga cagagcatat 360  
 ttgggaagaa acagtttgcc attgaatccc gtgtcatana atatccagca cagatgggtgg 420

tgttgatggt tagcaataan cacactctct cctttcgatg tgcattgtat antcaggtgg 480  
 atacaaaaag acatcgcttg gccacatgc aaggccaaaa agcagacatc agaaagagag 540  
 cagtcatgtg ggggaattgg tccgactgc 569

<210> 24  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> T7Rpol-N primer

<400> 24  
 atatttttagc catggaggat tgatatatga acacgattaa catcgctaag 50

<210> 25  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> T7Rpol-C primer

<400> 25  
 atatttttagc catggtatag tgagtcgtat tgatttggcg 40

<210> 26  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> F646Y(+) primer

<400> 26  
 gttgacggaa gccgtactct ttggac 26

<210> 27  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> F646Y(-) primer

<400> 27  
 gtccaaagag tacggcttcc gtcaac 26

<210> 28  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> T7RNAP-HpaI-N primer

<400> 28

cgcgcggtta acttgcttcc tag 23

<210> 29  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> pTrc99a-PstI-C primer

<400> 29  
 gcatgcctgc aggtcgactc tag 23

<210> 30  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> ApaF1 primer

<400> 30  
 catctggtcg cattgggtca c 21

<210> 31  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Xho-R primer

<400> 31  
 ccaagtgttc tcgagtggag a 21

<210> 32  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Xho-F primer

<400> 32  
 ctaagtctcc actcgagaac acttgg 26

<210> 33  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

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22

NCBI Protein

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Bio

Search  for

Limits Preview/Index History Clipboard Details

Show:

☐ 1: CAA26719. unnamed protein p...[gi:15562]

[BLink](#), [Domains](#), [Links](#)

LOCUS CAA26719 884 aa linear PHG 12-SEP-1993  
DEFINITION unnamed protein product [Bacteriophage T3].  
ACCESSION CAA26719  
VERSION CAA26719.1 GI:15562  
DBSOURCE embl locus PODOT3P, accession X02981.1  
KEYWORDS .  
SOURCE Bacteriophage T3  
ORGANISM Bacteriophage T3  
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
T7-like viruses.  
REFERENCE 1 (residues 1 to 884)  
AUTHORS McGraw,N.J., Bailey,J.N., Cleaves,G.R., Dembinski,D.R., Gocke,C.R.,  
Joliffe,L.K., MacWright,R.S. and McAllister,W.T.  
TITLE Sequence and analysis of the gene for bacteriophage T3 RNA  
polymerase  
JOURNAL Nucleic Acids Res. 13 (18), 6753-6766 (1985)  
MEDLINE 86041870  
PUBMED 3903658  
COMMENT Data kindly reviewed (5-MAR-1986) by McAllister W.T.

FEATURES Location/Qualifiers  
source 1..884  
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Protein 1..884  
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CDS 1..884  
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301 hskkglmrye dvympevyka vnlaqntawk inkkvavvn eivnwknpcv adipslerge
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Limits Preview/Index History Clipboard Details

Show:

☐ 1: CAA37330. unnamed protein p...[gi:14985]

[BLink](#), [Domains](#), [Links](#)

LOCUS CAA37330 906 aa linear PHG 12-SEP-1993  
DEFINITION unnamed protein product [Bacteriophage K11].  
ACCESSION CAA37330  
VERSION CAA37330.1 GI:14985  
DBSOURCE embl locus KSK11RPO, accession X53238.1  
KEYWORDS .  
SOURCE Bacteriophage K11  
ORGANISM Bacteriophage K11  
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.  
REFERENCE 1 (residues 1 to 906)  
AUTHORS Dietz,A., Weisser,H.J., Kossel,H. and Hausmann,R.  
TITLE The gene for Klebsiella bacteriophage K11 RNA polymerase: sequence and comparison with the homologous genes of phages T7, T3, and SP6  
JOURNAL Mol. Gen. Genet. 221 (2), 283-286 (1990)  
MEDLINE 90318328  
PUBMED 2370850  
REFERENCE 2 (residues 1 to 906)  
AUTHORS Hausmann,R.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUL-1990) Hausmann R., Institut Biologie III der Universitaet, Schaezlestrasse 1, D-7800 Freiburg, BRD  
COMMENT Data kindly reviewed (10-AUG-1990) by Hausmann R.  
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ORIGIN




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Search  for

Limits Preview/Index History Clipboard Details

Show:

☐ 1: CAA68288. unnamed protein p...[gi:15463]

[BLink](#), [Domains](#), [Links](#)

LOCUS CAA68288 874 aa linear PHG 12-SEP-1993

DEFINITION unnamed protein product [Enterobacteria phage Sf6].

ACCESSION CAA68288

VERSION CAA68288.1 GI:15463

DBSOURCE embl locus NCSP6RNP, accession Y00105.1

KEYWORDS .

SOURCE Enterobacteria phage Sf6

ORGANISM Enterobacteria phage Sf6

Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
P22-like viruses.

REFERENCE 1 (residues 1 to 874)

AUTHORS Kotani,H., Ishizaki,Y., Hiraoka,N. and Obayashi,A.

TITLE Nucleotide sequence and expression of the cloned gene of  
bacteriophage SP6 RNA polymerase

JOURNAL Nucleic Acids Res. 15 (6), 2653-2664 (1987)

MEDLINE 87174790

PUBMED 3031606

REFERENCE 2 (residues 1 to 874)

AUTHORS Kotani,H.

TITLE Direct Submission

JOURNAL Submitted (27-MAR-1987) Hirokaza Kotani, Central Research  
Laboratories, Takava Schuzo Coy LTD, Sera 3-4-1, Otsu, Schiza  
520-21, Japan

FEATURES Location/Qualifiers

source

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Protein

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841 eehevrrmvd tgievpegge fdlneimdse yvfa

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